IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application No:	09/972,268
Applicants:	Peter R. Baum, William C. Fanslow III, Timothy E. Lofton, Eric A. Sorensen, and Adel Youakim
Filed:	October 5, 2001
Title:	NECTIN POLYPEPTIDES
TC/Art Unit:	1644
Examiner:	Maher M. Haddad
Docket No.:	3101-A

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

DECLARATION UNDER 37 C.F.R. § 1.131

We, Peter R. Baum, William C. Fanslow III, Timothy E. Lofton, Eric A. Sorensen, and Adel Youakim, the undersigned, hereby declare that:

1. This Declaration is made by the inventors of the above-captioned patent application in order to establish a date of invention in the United States prior to April 1, 2000.

2. Prior to April 1, 2000, a DNA clone that encodes human nectin-3 polypeptide (also called "B7L4" polypeptide) had been isolated and its sequence determined in the United States by inventors named in the subject application, as evidenced by the Exhibits A and B enclosed herewith. The works described in Exhibits A and B were completed in this country prior to April 1, 2000.

3. Exhibit A is a copy of a page from one of the laboratory notebooks of Eric A. Sorensen, written in his handwriting, describing a restriction enzyme digest of an isolated lambda phage clone called "HuB7L4 11-1". All dates on the copy have been redacted.

4. Exhibit B (eight pages) is a copy of a computer printout that is incorporated into one of the laboratory notebooks of Eric A. Sorensen, showing the results of the sequencing of the HuB7L4 11-1 clone insert that was performed at the direction of Eric A. Sorensen. The amino acid sequence shown below the corresponding nucleotide sequences is that of human nectin-3 as presented in SEQ ID NO:2 of the above-captioned application (and is identical to amino acids 8 through 549 of SEQ ID NOs 4 and 6). The first page of Exhibit B indicates the location of a predicted signal sequence cleavage site, and the fourth page of Exhibit B indicates the location of the start of the transmembrane domain. All dates on the copy have been redacted.

5. Therefore, on a date prior to April 1, 2000, the inventors of the above-captioned application had determined the amino acid sequence of a human nectin-3 polypeptide including the extracellular domain of a mature form of human nectin-3.

6. As a person signing below: I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Peter R. Baum — Date: _____

William C. Fanslow III — Date: June 23, 2003

William C. Fanslow III

Timothy E. Lofton — Date: 23 JUNE 2003

Timothy E. Lofton

Eric A. Sorensen — Date: June 24, 2003

Eric A. Sorensen

Adel Youakim — Date: June 24, 2003

Adel Youakim

rom Page No. 77

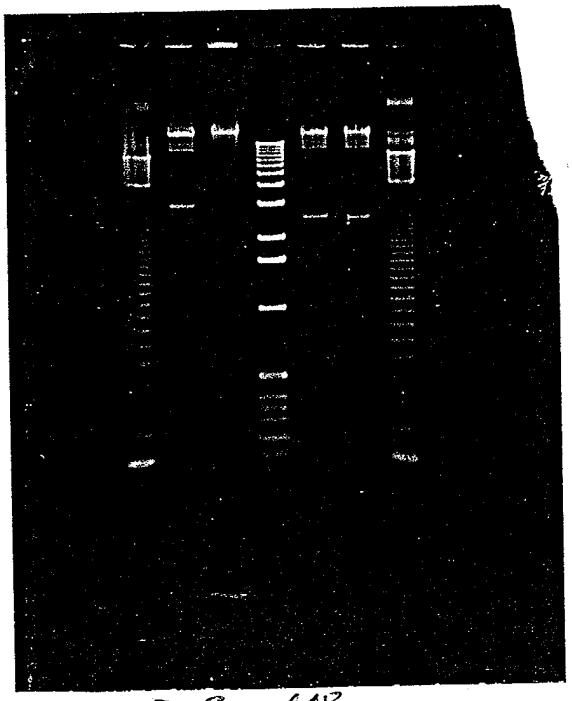
ØDNA for HuB7C4 picks 11-1 and 13 (from kB library) sat in PEG for the 3 weeks I was on vacation.
Spun out. Washed 1x w 70% EtOH. Spd vac'd 4 min heat. Resuspended o/n in 60 µl H_2O.

Digest ØDNAs w EcoRI (NEB rxn buffer) and w NotI (NEB buffer, BSA

1.)	ØDNA 11-1	w EcoRI	4 µl ØDNA
2.)	"	w NotI	1.5 µl 10x buffer
3.)	ØDNA 13	w EcoRI	.5 µl enzyme
4.)	"	NotI	9 µl H_2O

37°C 60-90'

#11-1 @ 95.5 µg/ml
#13 @ 57.7 µg/ml



7055 p 80 AMS

RESULTS:

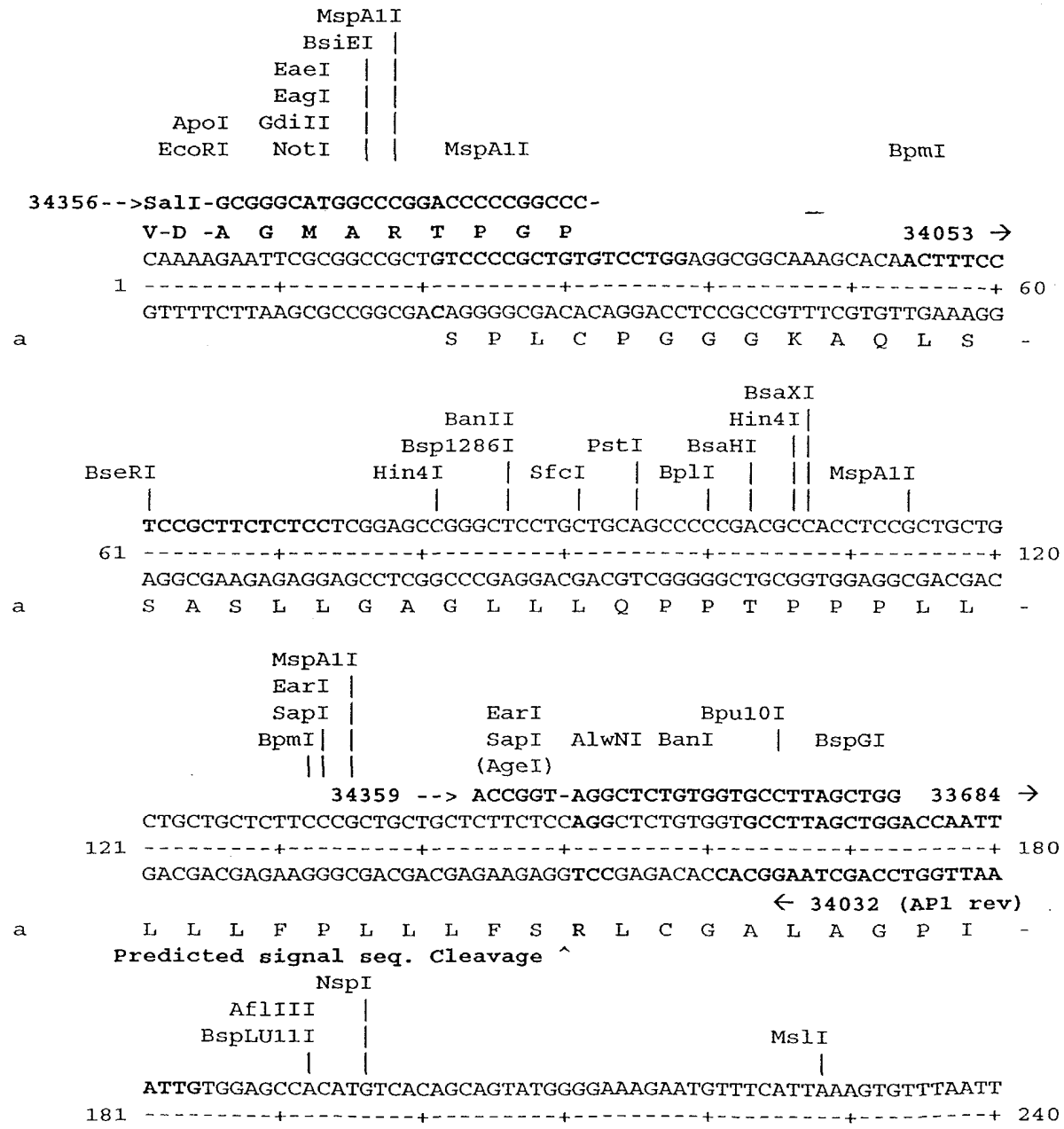
According to this gel, the clone #13 is way small compared to what I estimated by analog PCR. I guess I'll see what the DNA sequence is and I'm going to subclone the EcoRI fragment into pBS

To Page No. 8

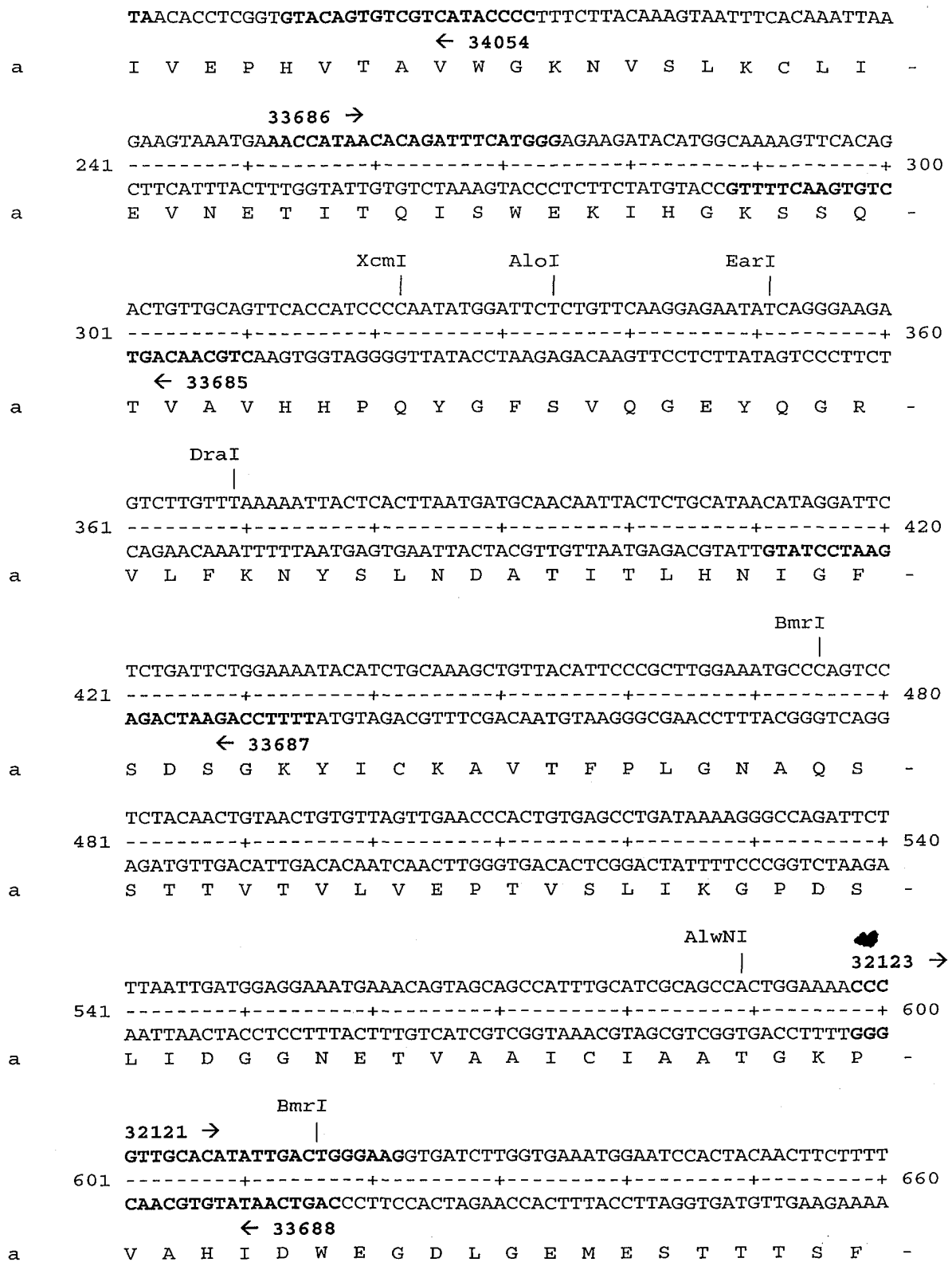
Witnessed & Understood by me,	Date	Invented by	Date
		Recorded by	

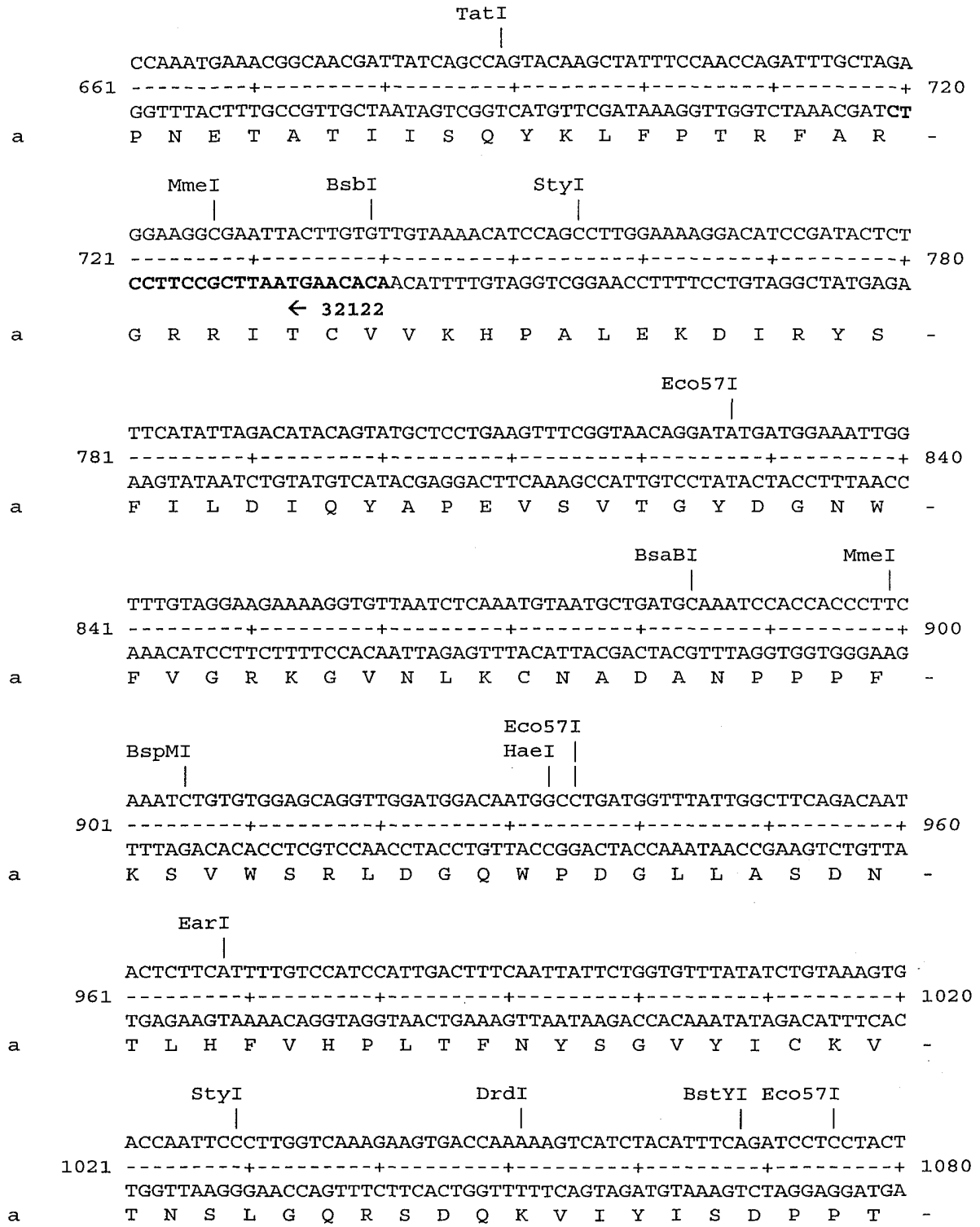
(Linear) (MinSite=6) MAP of: **hub7l4-11.seq** check: 8088 from: 1 to: 3187

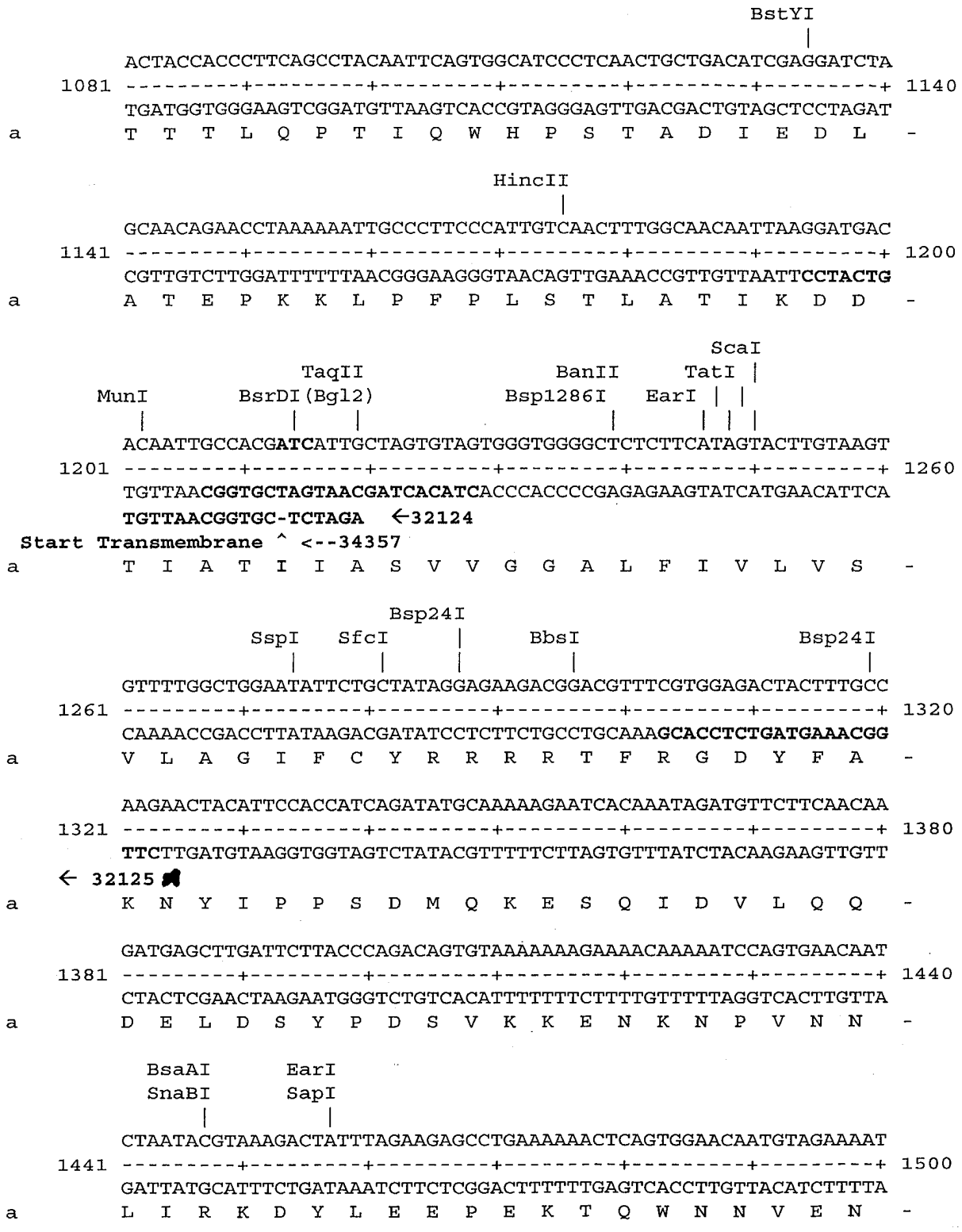
HuB7L4 #11 from KB library clone #11-1. Phage DNA: **NOT CONFIRMED**
sr6527 R. Sorensen
/bertlesj/sorensen/sr6527/hub7l4-11.seq
8139,8140,DPC#9117-20,12233-34,12759-60,12801
HuB7L4-11
With 164 enzymes: *

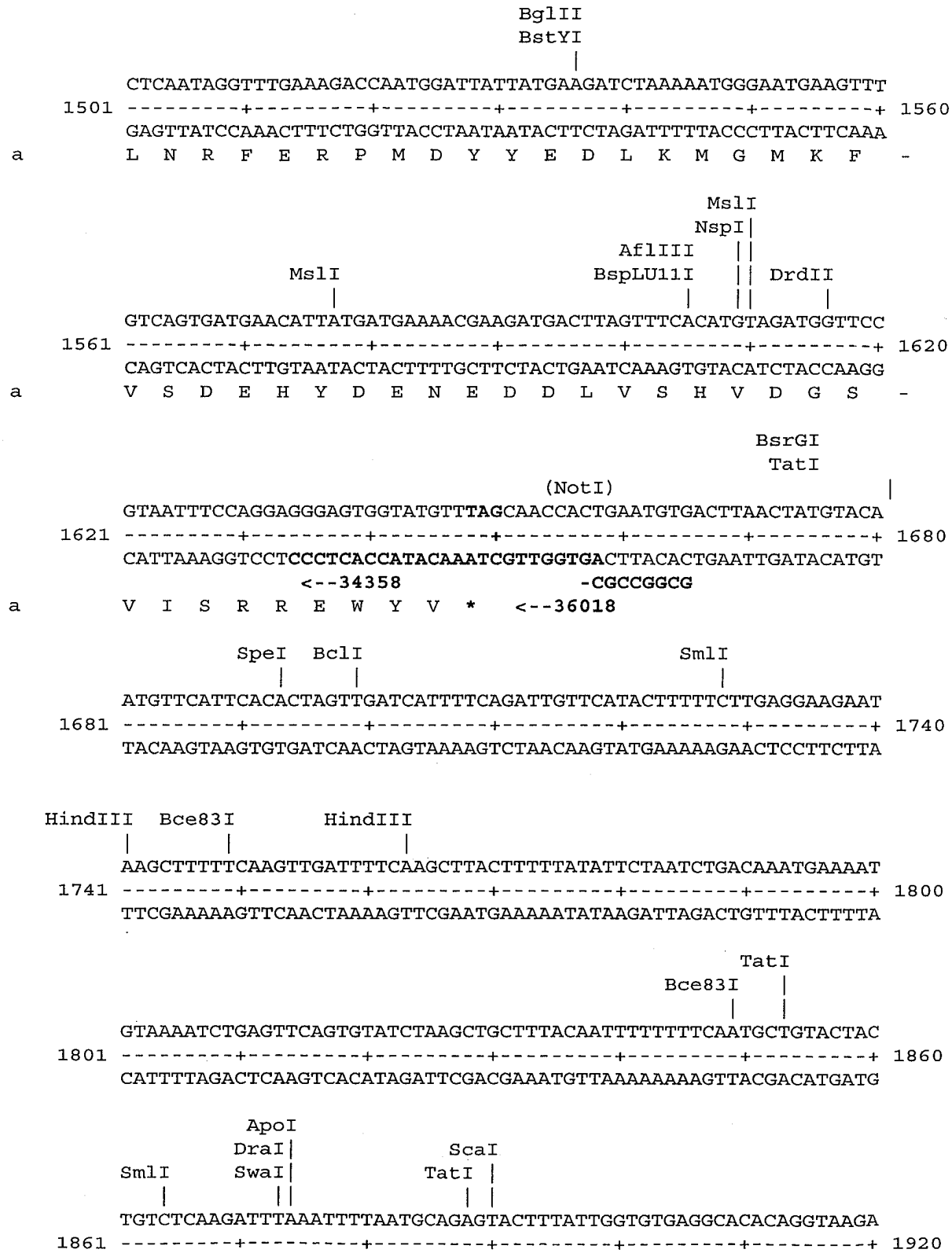


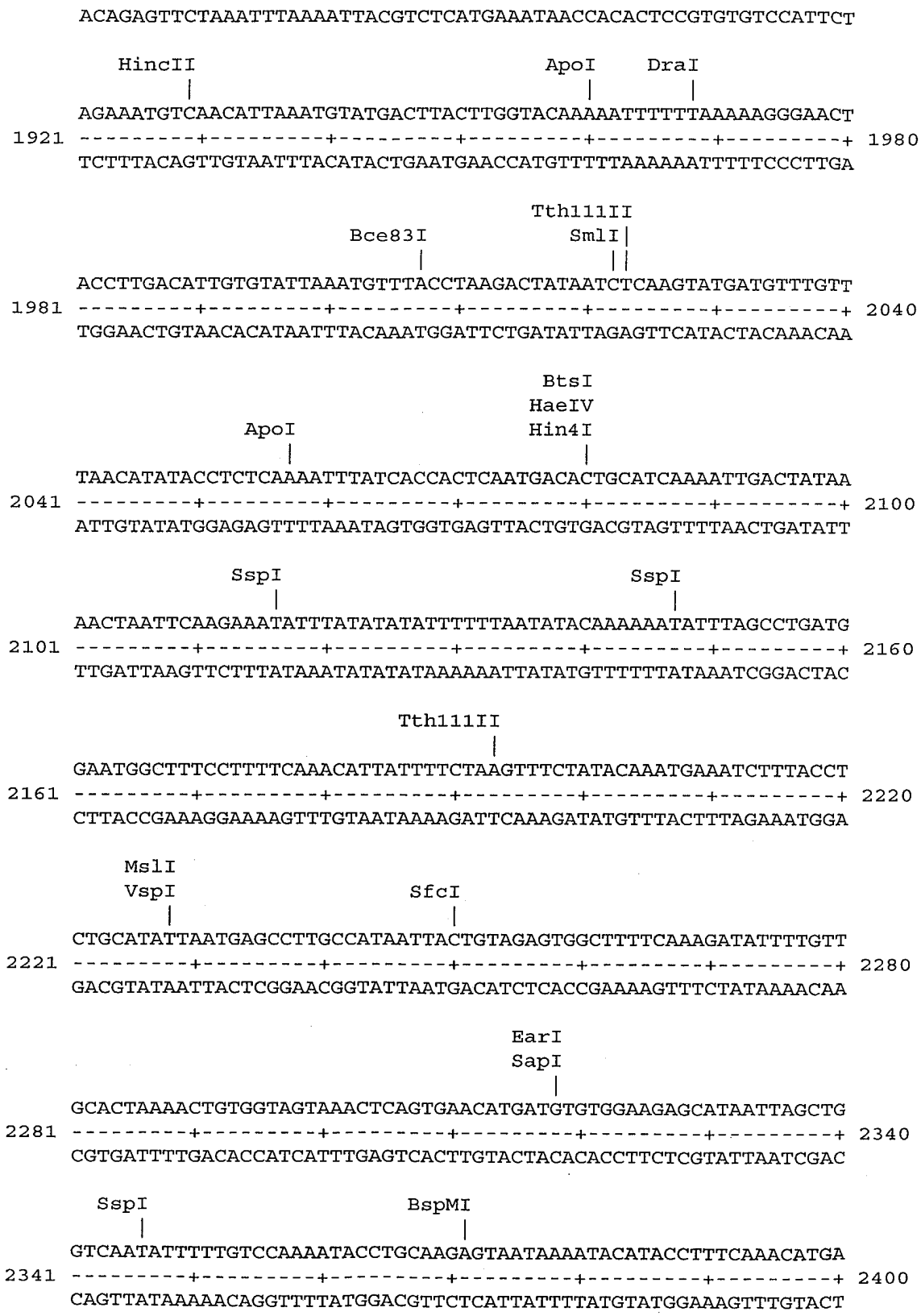
7785 p 8

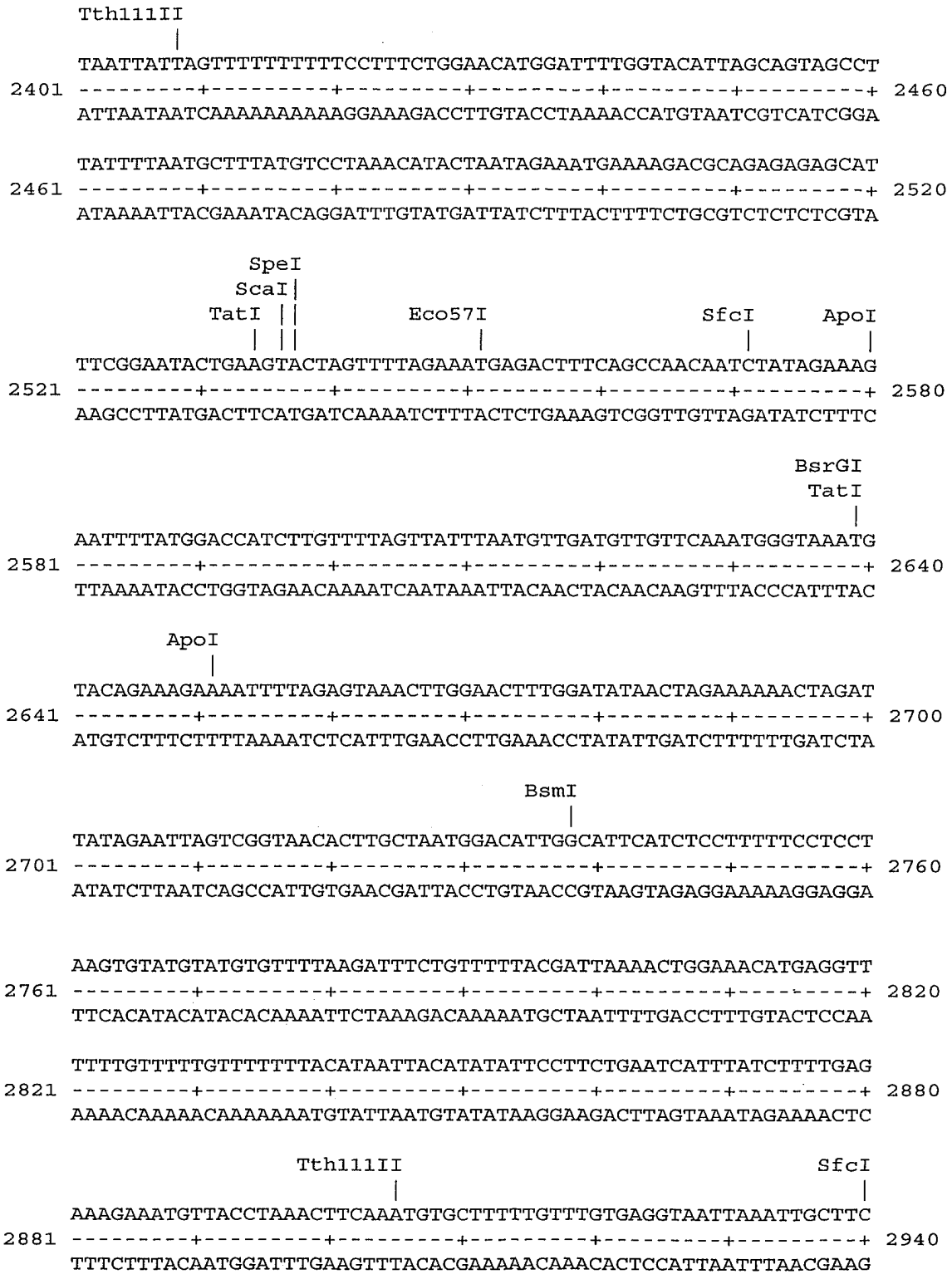

TAACACCTCGGTGTACAGTGTCGTCATACCCCTTTCTTACAAAGTAATTTCACAAATTAA
← 34054
a I V E P H V T A V W G K N V S L K C L I -
33686 →
GAAGTAAATGAAACCATAACACAGATTTCATGGGAGAAGATACATGGCAAAAGTTCACAG
241 ---------+---------+---------+---------+---------+---------+ 300
CTTCATTTACTTTGGTATTGTGTCTAAAGTACCCTCTTCTATGTACCGTTTTCAAGTGTC
a E V N E T I T Q I S W E K I H G K S S Q -
XcmI AloI EarI
ACTGTTGCAGTTCACCATCCCCAATATGGATTCTCTGTTCAAGGAGAATATCAGGGAAGA
301 ---------+---------+---------+---------+---------+---------+ 360
TGACAACGTCAAGTGGTAGGGGTTATACCTAAGAGACAAGTTCCTCTTATAGTCCCTTCT
← 33685
a T V A V H H P Q Y G F S V Q G E Y Q G R -
DraI
GTCTTGTTTAAAAATTACTCACTTAATGATGCAACAATTACTCTGCATAACATAGGATTC
361 ---------+---------+---------+---------+---------+---------+ 420
CAGAACAAATTTTTAATGAGTGAATTACTACGTTGTTAATGAGACGTATTGTATCCTAAG
a V L F K N Y S L N D A T I T L H N I G F -
BmrI
TCTGATTCTGGAAAATACATCTGCAAAGCTGTTACATTCCCGCTTGGAAATGCCCAGTCC
421 ---------+---------+---------+---------+---------+---------+ 480
AGACTAAGACCTTTTATGTAGACGTTTCGACAATGTAAGGGCGAACCTTTACGGGTCAGG
← 33687
a S D S G K Y I C K A V T F P L G N A Q S -
TCTACAACTGTAACTGTGTTAGTTGAACCCACTGTGAGCCTGATAAAAGGGCCAGATTCT
481 ---------+---------+---------+---------+---------+---------+ 540
AGATGTTGACATTGACACAATCAACTTGGGTGACACTCGGACTATTTTCCCGGTCTAAGA
a S T T V T V L V E P T V S L I K G P D S -
AlwNI
32123 →
TTAATTGATGGAGGAAATGAAACAGTAGCAGCCATTTGCATCGCAGCCACTGGAAAACCC
541 ---------+---------+---------+---------+---------+---------+ 600
AATTAACTACCTCCTTTACTTTGTCATCGTCGGTAAACGTAGCGTCGGTGACCTTTTGGG
a L I D G G N E T V A A I C I A A T G K P -
BmrI
32121 →
GTTGCACATATTGACTGGGAAGGTGATCTTGGTGAAATGGAATCCACTACAACTTCTTTT
601 ---------+---------+---------+---------+---------+---------+ 660
CAACGTGTATAACTGACCCTTCCACTAGAACCACTTTACCTTAGGTGATGTTGAAGAAAA
← 33688
a V A H I D W E G D L G E M E S T T T S F -


TatI
CCAAATGAAACGGCAACGATTATCAGCCAGTACAAGCTATTTCCAACCAGATTTGCTAGA
661 ---------+---------+---------+---------+---------+---------+ 720
GGTTTACTTTGCCGTTGCTAATAGTCGGTCATGTTCGATAAAGGTTGGTCTAAACGATCT
a P N E T A T I I S Q Y K L F P T R F A R -
MmeI
BsbI
StyI
GGAAGGCGAATTACTTGTGTTGTAAAACATCCAGCCTTGGAAAAGGACATCCGATACTCT
721 ---------+---------+---------+---------+---------+---------+ 780
CCTTCCGCTTAATGAACACAACATTTTGTAGGTCGGAACCTTTTCCTGTAGGCTATGAGA
← 32122
a G R R I T C V V K H P A L E K D I R Y S -
Eco57I
TTCATATTAGACATACAGTATGCTCCTGAAGTTTCGGTAACAGGATATGATGGAAATTGG
781 ---------+---------+---------+---------+---------+---------+ 840
AAGTATAATCTGTATGTCATACGAGGACTTCAAAGCCATTGTCCTATACTACCTTTAACC
a F I L D I Q Y A P E V S V T G Y D G N W -
BsaBI
MmeI
TTTGTAGGAAGAAAAGGTGTTAATCTCAAATGTAATGCTGATGCAAATCCACCACCCTTC
841 ---------+---------+---------+---------+---------+---------+ 900
AAACATCCTTCTTTTCCACAATTAGAGTTTACATTACGACTACGTTTAGGTGGTGGGAAG
a F V G R K G V N L K C N A D A N P P P F -
Eco57I
BspMI
HaeI
AAATCTGTGTGGAGCAGGTTGGATGGACAATGGCCTGATGGTTTATTGGCTTCAGACAAT
901 ---------+---------+---------+---------+---------+---------+ 960
TTTAGACACACCTCGTCCAACCTACCTGTTACCGGACTACCAAATAACCGAAGTCTGTTA
a K S V W S R L D G Q W P D G L L A S D N -
EarI
ACTCTTCATTTTGTCCATCCATTGACTTTCAATTATTCTGGTGTTTATATCTGTAAAGTG
961 ---------+---------+---------+---------+---------+---------+ 1020
TGAGAAGTAAAACAGGTAGGTAACTGAAAGTTAATAAGACCACAAATATAGACATTTCAC
a T L H F V H P L T F N Y S G V Y I C K V -
StyI
DrdI
BstYI
Eco57I
ACCAATTCCCTTGGTCAAAGAAGTGACCAAAAAGTCATCTACATTTCAGATCCTCCTACT
1021 ---------+---------+---------+---------+---------+---------+ 1080
TGGTTAAGGGAACCAGTTTCTTCACTGGTTTTTCAGTAGATGTAAAGTCTAGGAGGATGA
a T N S L G Q R S D Q K V I Y I S D P P T -


BstYI
ACTACCACCCTTCAGCCTACAATTCAGTGGCATCCCTCAACTGCTGACATCGAGGATCTA
1081
1140
TGATGGTGGGAAGTCGGATGTTAAGTCACCGTAGGGAGTTGACGACTGTAGCTCCTAGAT
a T T T L Q P T I Q W H P S T A D I E D L -
HincII
GCAACAGAACCTAAAAAATTGCCCTTCCCATTGTCAACTTTGGCAACAATTAAGGATGAC
1141
1200
CGTTGTCTTGGATTTTTTAACGGGAAGGGTAACAGTTGAAACCGTTGTTAATTCCTACTG
a A T E P K K L P F P L S T L A T I K D D -
ScaI
TaqII
BanII
TatI
MunI
BsrDI(Bgl2)
Bsp1286I
EarI
ACAATTGCCACGATCATTGCTAGTGTAGTGGGTGGGGCTCTCTTCATAGTACTTGTAAGT
1201
1260
TGTTAACGGTGCTAGTAACGATCACATCACCCACCCCGAGAGAAGTATCATGAACATTCA
TGTTAACGGTGC-TCTAGA ←32124
Start Transmembrane ^ <--34357
a T I A T I I A S V V G G A L F I V L V S -
Bsp24I
SspI
SfcI
BbsI
Bsp24I
GTTTTGGCTGGAATATTCTGCTATAGGAGAAGACGGACGTTTCGTGGAGACTACTTTGCC
1261
1320
CAAAACCGACCTTATAAGACGATATCCTCTTCTGCCTGCAAAGCACCTCTGATGAAACGG
a V L A G I F C Y R R R R T F R G D Y F A -
AAGAACTACATTCCACCATCAGATATGCAAAAAGAATCACAAATAGATGTTCTTCAACAA
1321
1380
TTCTTGATGTAAGGTGGTAGTCTATACGTTTTTCTTAGTGTTTATCTACAAGAAGTTGTT
← 32125
a K N Y I P P S D M Q K E S Q I D V L Q Q -
GATGAGCTTGATTCTTACCCAGACAGTGTAAAAAAAGAAAACAAAAATCCAGTGAACAAT
1381
1440
CTACTCGAACTAAGAATGGGTCTGTCACATTTTTTTCTTTTGTTTTTAGGTCACTTGTTA
a D E L D S Y P D S V K K E N K N P V N N -
BsaAI
SnaBI
EarI
SapI
CTAATACGTAAAGACTATTTAGAAGAGCCTGAAAAAACTCAGTGGAACAATGTAGAAAAT
1441
1500
GATTATGCATTTCTGATAAATCTTCTCGGACTTTTTTGAGTCACCTTGTTACATCTTTTA
a L I R K D Y L E E P E K T Q W N N V E N -


BglII
BstYI
CTCAATAGGTTTGAAAGACCAATGGATTATTATGAAGATCTAAAAATGGGAATGAAGTTT
1501
1560
GAGTTATCCAAACTTTCTGGTTACCTAATAATACTTCTAGATTTTTACCCTTACTTCAAA
a L N R F E R P M D Y Y E D L K M G M K F -
MslI
NspI
AflIII
MslI
BspLU11I
DrdII
GTCAGTGATGAACATTATGATGAAAACGAAGATGACTTAGTTTCACATGTAGATGGTTCC
1561
1620
CAGTCACTACTTGTAATACTACTTTTGCTTCTACTGAATCAAAGTGTACATCTACCAAGG
a V S D E H Y D E N E D D L V S H V D G S -
BsrGI
TatI
(NotI)
GTAATTTCCAGGAGGGAGTGGTATGTTTAGCAACCACTGAATGTGACTTAACTATGTACA
1621
1680
CATTAAAGGTCCTCCCTCACCATACAAATCGTTGGTGACTTACACTGAATTGATACATGT
<--34358
-CGCCGGCG
a V I S R R E W Y V * <--36018
SpeI
BclI
SmlI
ATGTTCATTCACACTAGTTGATCATTTTCAGATTGTTCATACTTTTTCTTGAGGAAGAAT
1681
1740
TACAAGTAAGTGTGATCAACTAGTAAAAGTCTAACAAGTATGAAAAAGAACTCCTTCTTA
HindIII
Bce83I
HindIII
AAGCTTTTTCAAGTTGATTTTCAAGCTTACTTTTTATATTCTAATCTGACAAATGAAAAT
1741
1800
TTCGAAAAAGTTCAACTAAAAGTTCGAATGAAAAATATAAGATTAGACTGTTTACTTTTA
TatI
Bce83I
GTAAAATCTGAGTTCAGTGTATCTAAGCTGCTTTACAATTTTTTTTCAATGCTGTACTAC
1801
1860
CATTTTAGACTCAAGTCACATAGATTCGACGAAATGTTAAAAAAAAGTTACGACATGATG
ApoI
DraI
ScaI
SmlI
SwaI
TatI
TGTCTCAAGATTTAAATTTTAATGCAGAGTACTTTATTGGTGTGAGGCACACAGGTAAGA
1861
1920


ACAGAGTTCTAAATTTAAAATTACGTCTCATGAAATAACCACACTCCGTGTGTCCATTCT
HincII
ApoI
DraI
AGAAATGTCAACATTAAATGTATGACTTACTTGGTACAAAAATTTTTTAAAAAGGGAACT
1921 ---------+---------+---------+---------+---------+---------+ 1980
TCTTTACAGTTGTAATTTACATACTGAATGAACCATGTTTTTAAAAAATTTTTCCCTTGA
Tth111II
Bce83I
SmlI
ACCTTGACATTGTGTATTAAATGTTTACCTAAGACTATAATCTCAAGTATGATGTTTGTT
1981 ---------+---------+---------+---------+---------+---------+ 2040
TGGAACTGTAACACATAATTTACAAATGGATTCTGATATTAGAGTTCATACTACAAACAA
BtsI
HaeIV
ApoI
Hin4I
TAACATATACCTCTCAAAATTTATCACCACTCAATGACACTGCATCAAAATTGACTATAA
2041 ---------+---------+---------+---------+---------+---------+ 2100
ATTGTATATGGAGAGTTTTAAATAGTGGTGAGTTACTGTGACGTAGTTTTAACTGATATT
SspI
SspI
AACTAATTCAAGAAATATTTATATATATTTTTTAATATACAAAAAATATTTAGCCTGATG
2101 ---------+---------+---------+---------+---------+---------+ 2160
TTGATTAAGTTCTTTATAAATATATATAAAAAATTATATGTTTTTTATAAATCGGACTAC
Tth111II
GAATGGCTTTCCTTTTCAAACATTATTTTCTAAGTTTCTATACAAATGAAATCTTTACCT
2161 ---------+---------+---------+---------+---------+---------+ 2220
CTTACCGAAAGGAAAAGTTTGTAATAAAAGATTCAAAGATATGTTTACTTTAGAAATGGA
MslI
VspI
SfcI
CTGCATATTAATGAGCCTTGCCATAATTACTGTAGAGTGGCTTTTCAAAGATATTTTGTT
2221 ---------+---------+---------+---------+---------+---------+ 2280
GACGTATAATTACTCGGAACGGTATTAATGACATCTCACCGAAAAGTTTCTATAAAACAA
EarI
SapI
GCACTAAAACTGTGGTAGTAAACTCAGTGAACATGATGTGTGGAAGAGCATAATTAGCTG
2281 ---------+---------+---------+---------+---------+---------+ 2340
CGTGATTTTGACACCATCATTTGAGTCACTTGTACTACACACCTTCTCGTATTAATCGAC
SspI
BspMI
GTCAATATTTTTGTCCAAAATACCTGCAAGAGTAATAAAATACATACCTTTCAAACATGA
2341 ---------+---------+---------+---------+---------+---------+ 2400
CAGTTATAAAAACAGGTTTTATGGACGTTCTCATTATTTTATGTATGGAAAGTTTGTACT


Tth111II
TAATTATTAGTTTTTTTTTTCCTTTCTGGAACATGGATTTTGGTACATTAGCAGTAGCCT
2401 ---------+---------+---------+---------+---------+---------+ 2460
ATTAATAATCAAAAAAAAAAGGAAAGACCTTGTACCTAAAACCATGTAATCGTCATCGGA
TATTTTAATGCTTTATGTCCTAAACATACTAATAGAAATGAAAAGACGCAGAGAGAGCAT
2461 ---------+---------+---------+---------+---------+---------+ 2520
ATAAAATTACGAAATACAGGATTTGTATGATTATCTTTACTTTTCTGCGTCTCTCTCGTA
SpeI
ScaI
TatI
Eco57I
SfcI
ApoI
TTCGGAATACTGAAGTACTAGTTTTAGAAATGAGACTTTCAGCCAACAATCTATAGAAAG
2521 ---------+---------+---------+---------+---------+---------+ 2580
AAGCCTTATGACTTCATGATCAAAATCTTTACTCTGAAAGTCGGTTGTTAGATATCTTTC
BsrGI
TatI
AATTTTATGGACCATCTTGTTTTAGTTATTTAATGTTGATGTTGTTCAAATGGGTAAATG
2581 ---------+---------+---------+---------+---------+---------+ 2640
TTAAAATACCTGGTAGAACAAAATCAATAAATTACAACTACAACAAGTTTACCCATTTAC
ApoI
TACAGAAAGAAAATTTTAGAGTAAACTTGGAACTTTGGATATAACTAGAAAAAACTAGAT
2641 ---------+---------+---------+---------+---------+---------+ 2700
ATGTCTTTCTTTTAAAATCTCATTTGAACCTTGAAACCTATATTGATCTTTTTTGATCTA
BsmI
TATAGAATTAGTCGGTAACACTTGCTAATGGACATTGGCATTCATCTCCTTTTTCCTCCT
2701 ---------+---------+---------+---------+---------+---------+ 2760
ATATCTTAATCAGCCATTGTGAACGATTACCTGTAACCGTAAGTAGAGGAAAAAGGAGGA
AAGTGTATGTATGTGTTTTAAGATTTCTGTTTTTACGATTAAAACTGGAAACATGAGGTT
2761 ---------+---------+---------+---------+---------+---------+ 2820
TTCACATACATACACAAAATTCTAAAGACAAAAATGCTAATTTTGACCTTTGTACTCCAA
TTTTGTTTTTGTTTTTTTACATAATTACATATATTCCTTCTGAATCATTTATCTTTTGAG
2821 ---------+---------+---------+---------+---------+---------+ 2880
AAAACAAAAACAAAAAAATGTATTAATGTATATAAGGAAGACTTAGTAAATAGAAAACTC
Tth111II
SfcI
AAAGAAATGTTACCTAAACTTCAAATGTGCTTTTTGTTTGTGAGGTAATTAAATTGCTTC
2881 ---------+---------+---------+---------+---------+---------+ 2940
TTTCTTTACAATGGATTTGAAGTTTACACGAAAAACAAACACTCCATTAATTTAACGAAG

```
     TACAGTGGAGGCTTACAAAATTATTGTGACAACTATTTTGAAGCTGAAAGGATAGTTTTT
2941 ---------+---------+---------+---------+---------+---------+ 3000
     ATGTCACCTCCGAATGTTTTAATAACACTGTTGATAAAACTTCGACTTTCCTATCAAAAA

     CTATTGCTAAGTCATTTGAAAAAGTGACCATTTTGCCAGTGAAATGAAGTGGAAGTTAGT
3001 ---------+---------+---------+---------+---------+---------+ 3060
     GATAACGATTCAGTAAACTTTTTCACTGGTAAAACGGTCACTTTACTTCACCTTCAATCA

     AGGAGAATCATAAATTAAATATATTATTTTGTTAATAAAAAGGCAAAGTAGTAGGTACTT
3061 ---------+---------+---------+---------+---------+---------+ 3120
     TCCTCTTAGTATTTAATTTATATAATAAAACAATTATTTTTCCGTTTCATCATCCATGAA

                                                              ApoI
                                                             EcoRI
                                                       BsiEI    |
                                                     EaeI  |    |
                                                     EagI  |    |
                                                    GdiII  |    |
                                                     NotI  |    |
     DraI                          SspI            MspA1I|   |    |
       |                             |                 ||   |    |
     TTTAAACCCTCCCAACCAGCCCTTTCTCAATATTCATCAAATCTAAAACAGCGGCCGCGA
3121 ---------+---------+---------+---------+---------+---------+ 3180
     AAATTTGGGAGGGTTGGTCGGGAAAGAGTTATAAGTAGTTTAGATTTTGTCGCCGGCGCT

     ATTCAGC
3181 ------- 3187
     TAAGTCG
```

Enzymes that do cut:

AflIII	AloI	AlwNI	ApoI	BanI	BanII	BbsI	Bce83I
BclI	BglII	BmrI	BplI	BpmI	Bpu10I	BsaAI	BsaBI
BsaHI	BsaXI	BsbI	BseRI	BsiEI	BsmI	Bsp24I	Bsp1286I
BspGI	BspLU11I	BspMI	BsrDI	BsrGI	BstYI	BtsI	DraI
DrdI	DrdII	EaeI	EagI	EarI	Eco57I	EcoRI	GdiII
HaeI	HaeIV	Hin4I	HincII	HindIII	MmeI	MslI	MspA1I
MunI	NotI	NspI	PstI	SapI	ScaI	SfcI	SmlI
SnaBI	SpeI	SspI	StyI	SwaI	TaqII	TatI	Tth111II
VspI	XcmI						

Enzymes that do not cut:

AarI	AatII	AccI	AceIII	AclI	AflII	AhdI	ApaI
ApaLI	AscI	AvaI	AvrII	BaeI	BamHI	BbvCI	BcgI
BciVI	BglI	BmgI	Bpu1102I	BsaI	BsaWI	BseSI	BsgI
BsiHKAI	BsmBI	BspEI	BsrBI	BsrFI	BssHII	BsssI	BstAPI
BstDSI	BstEII	BstXI	BstZ17I	Bsu36I	ClaI	DraIII	EciI
Eco47III	EcoNI	Eco0109I	EcoRV	FseI	FspI	HaeII	HgiEII
HpaI	KpnI	MluI	MscI	NarI	NcoI	NdeI	NgoAIV
NheI	NruI	NsiI	NspV	PacI	Pfl1108I	PflMI	PinAI
PmeI	PmlI	PpiI	PshAI	Psp5II	PvuI	PvuII	RcaI
RleAI	RsrII	SacI	SacII	SalI	SanDI	SbfI	SexAI
SfiI	SgfI	SgrAI	SmaI	SphI	SrfI	Sse8647I	StuI
SunI	Tth111I	XbaI	XhoI	XmnI			